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FIG. 1

FS-HBPI

T3→
1 AGAAAGCCAACATGAAGCTTCTGCTCTCTCTTGCCTTCGTCTTAGCTCTCAGCCAAGTTA 60
M K L L L S L A F V L A L S Q V K

61 AAGCCGATAAGCCAGTTTGGGCGGATGAAGCGGCAACGGGGAACACCAAGACGCTTGA 120
A D K P V W A D E A A N G E H Q D A W K
↑

121 AGCATCTCCAAAACTCGTTGAAGAGAATTACGACTTGATAAAAGCCACCTACAAGAAGC 180
H L Q K L V E E N Y D L I K A T Y K N D

181 ACCCAGTTTGGGSTAACGACTTCACTTGCCTGGGTACTGCAGCGCAGAATTTGAACGAGG 240
P V W G N D F T C V G T A A Q N L N E D
T3a→←T7c

241 ACGAGAAGAACGTTGAAGCATGGTTTATGTTTATGAATAATGCTGATACCGTATACCAAC 300
E K N V E A W F M F M N N A D T V Y Q H

301 ATACTTTTGAAGAGGCGACTCCTGATAAATGTACGGTTACAATAAGGAAAACGCCATCA 360
T F E K A T P D K M Y G Y N K E N A I T

361 CATATCAAACAGAGGATGGGCAAGTTCTCACAGACGTCCTTGCATTCTCTGACGACAATT 420
Y Q T E D G Q V L T D V L A F S D D N C

421 GCTATGTCATCTACGCTCTTGGCCCAAGTGGAGCAGSTTACGAACTCTGGGCTA 480
Y V I Y A L G P D G S G A G Y E L W A T

481 CCGATTACCGGATGTTCCAGCCAGTTGTCTAGAGAAGTTCAATGAGTATGCTGCAGGTC 540
D Y T D V P A S C L E K F N E Y A A G L
T3b→←T7d

541 TGCCGGTACGGGACGTATACACAAGTGATTGCCTCCCAGAATAACTTGGGCATATCGTAA 600
P V R D V Y T S D C L P E

601 TTTCAACTTCAAAGTGTGTTATTGTGTCAGCATATGCTCTCGAGTGTGTTGATGTAGTSCGTTT 660

661 GATGATGCCATTTCATCTAGSTTTGGGTTGTTGGTACTTTATGSTCACTGCCGACGGCCA 720

721 GCACGAGTACTCGAAATTAAGTATTCTGAAATCGGAAAAAAAAAAAAA 770
←T7

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FIG. 2

FS-HBP2

T3→

1	GCCGCGACGGAACCTTCGAAGGAAGTCAGCATGAAGCTTCTCATACTCTCTCTTGGCCCTCG	60
	M K L L I L S L A L V	
61	TCCTCGCCCTCAGCCAGGTTAAGGGAAATCAGCCAGATTGGGCCGATGAAGCGGCAAATG	120
	L A L S Q V K G <u>N Q P D W A D E A A N G</u>	
	↑	
121	GTGCACACCAAGACGCCTGGAAGAGTCTGAAAGCGGACGTTGAAAACGTTTACTACATGG	180
	A H Q D A W K S L K A D V E N V Y Y M V	
181	TGAAGGCCACCTATAAGAATGACCCAGTGTGGGGCAATGACTTCACTTGCGTGGGTGTTA	240
	K A T Y K N D P V W G N D F T C V G V M	
	T3b → ← T7a	
241	TGGCAAATGATGTCAACGAGGATGAGAAGAGCATTCAAGCAGAGTTTTTGTATTGAATA	300
	A N D V N E D E K S I Q A E F L F M N N	
301	ATGCTGACACAAACATGCAATTCGCCACTGAAAAGGTGACTGCTGTAAAATGTATGGTT	360
	A D T N M Q F A T E K V T A V K M Y G Y	
361	ACAATAGGGAAAACGCCTTCAGATACGAGACGGAGGATGGCCAAGTTTTACAGACGTCA	420
	N R E N A F R Y E T E D G Q V F T D V I	
	→	
421	TTGCATACTCTGATGACAACTGCGATGTCTATCTACGTTCTTGGCCAGACGGAAATGAGG	480
	A Y S D D N C D V I Y V P G T D G N E E	
	←	
481	AAGGTTACGAACTATGGACTACGGATTACGACAACATTCAGCCAATTGTTTTAAATAAGT	540
	G Y E L W T T D Y D N I P A N C L N K F	
541	TTAATGAGTACGCTGTAGGTAGGGAGACAAGGSATGTATTCACAAGTGCTTGCCTAGAGT	600
	N E Y A V G R E T R D V F T S A C L E	
	→	
601	<u>AATAACTTCAGAAATGTCGTTCTTTCAAAGCGAAAAACCAACAATGTGAACATCGGCTTGC</u>	660
661	TGTGCTCGACGTAGCCAGCGATAATGTTGTTTTCTGGGTTTCTGGGTTTGGATACTTTT	720
721	AGCCACTGCCGAAGAGCTGTAAGGTAATGAAAAATAAATGTTCAAGAGTGTGAAAAAA	780
	← T7	
781	AAAAAAAAAAAAA 793	

[illegible]

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FIG. 3

MS-HBPI

T3→		
1	AAAGCACTCAACATGAAGGTTCTTTTGGTTGGTTCTTGGAGCTGCTCTTTGCCAGAATGCA	60
	M K V L L L V L G A A L C Q N A	
61	GATGCAAACCCCAACATGGGSCGAACGAAGCTAAATTGGGATCCTACCAAGACGCCTGGAAG	120
	D A N P T W A N E A K L G S Y Q D A W K	
	↑	
121	AGCCTTCAGCAAGACCAAAACAAGAGATACTATTGTCACAAGCGACACAAACGACTGAC	180
	S L Q Q D Q N K R Y Y L A Q A T Q T T D	
181	GGCGTATGGGGTGAAGAGTTTACTTGTGTGAGTGTACGGTGTGAGAAGATTGGAAGAAA	240
	G V W G E E F T C V S V T A E K I G K K	
	→	
241	AACTTAACGCTACGATCCTCTATAAAAATAAGCACCTTACTGACCTGAAAGAGAGTCAT	300
	K L N A T I L Y K N K H L T D L K E S H	
	←	
301	GAAACAATCACTGTCTGGAAAGCATACGACTACACAACGGAGAATGGCATCAAGTACGAG	360
	E T I T V W K A Y D Y T T E N G I K Y E	
361	ACGCAAGGGACAAGGACGCGAGCTTTCGAAGATGTCTTTGTATTCTCTGATTACAAGAAC	420
	T Q G T R T Q T F E D V F V F S D Y K N	
421	TGCGATGTAATTTTCGTTCCCAAAGAGAGAGGAAGCGACGAGGGCGACTATGAATTGTGG	480
	C D V I F V P K E R G S D E G D Y E L W	
	→	
481	GTTAGTGAAGACAAGATTGACAAGATTCCCGATTGCTGCAAGTTTACGATGGCGTACTTT	540
	V S E D K I D K I P D C C K F T M A Y F	
541	GCCCAACAGCAGGAGAAGACGGTTTCGTAATGTATACACTGACTCATCATGCAAACCAGCA	600
	A Q Q Q E K T V R N V Y T D S S C K P A	
601	CCAGCTCAGAACTGATATTCTGTAATGCTTGAACCGTAATGTTTCGACCTGCAGTCTAG	660
	P A Q N	
661	AAACATTTACCACCATCACGGTGATTATCTTACCGTAGTTTCTTAGGTCTTCTCTTTG	720
	←T7	
721	ATAAAATAGTTCCCTGCATTGACAAAAA	753

[illegible]

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FIG. 4

T3→

1 ATGAAGATGCAGGTAGTGCTCTTACTTACCTTTGTTAGCGCCGCCCTCGCCACTCAAGCG 60
1 M K M Q V V L L L T F V S A A L A T Q A 20

61 GAGACTACATCTGCGAAAGCAGGAGAAAACCCGCTCTGGGCGCATGAGGAACTACTTGGG 120
21 E T T S A K A G E N P L W A H E E L L G 40
↑

121 AAATATCAAGATGCCTGGAAAAGCATCGATCAGGGCGTGTGCGGTGACTTATGTCCTTGCA 180
41 K Y Q D A W K S I D Q G V S V T Y V L A 60

181 AAGACAACATATGAGAATGACACAGGATCATGGGGATCCCAGTTTAAGTGCCTCCAGGTA 240
61 K T T Y E N D T G S W G S Q F K C L Q V 80
→ ←

241 CAAGAAATAGAAAGAAAGGAAGAAGACTATACAGTTACATCTGTTTTACCTTTAGAAAT 300
81 Q E I E R K E E D Y T V T S V F T F R N 100

301 GCGTCTTCTCCAATCAAGTATTACAACGTGACAGAAACAGTGAAGGCCGTTTTTCAATAT 360
101 A S S P I K Y Y N V T E T V K A V F Q Y 120

361 GGATACAAAAACATAAGGAATGCAATTGAATACCAAGTGGGCGGTGGACTTAACATAACC 420
121 G Y K N I R N A I E Y Q V G G G L N I T 140

421 GACACGCTCATTTTTCACTGATGGAGAATTATGCGATGTTTTCTATGTTCCCAATGCAGAT 480
141 D T L I F T D G E L C D V F Y V P N A D 160
→ ←

481 CAAGGTTGTGAGCTCTGGGTCAAAAAGAGTCACTACAAACACGTACCAGACTACTGCACG 540
161 Q G C E L W V K K S H Y K H V P D Y C T 180

541 TTCGTGTTCAATGTTTTCTGTGCGAAAGACAGGAAAACCTACGATATATTTAATGAAGAA 600
181 F V F N V F C A K D R K T Y D I F N E E 200

601 TGTGTTTATAACGGCGAACCCCTGGCTTTAAAGGCCAAAAATCTATAAAATACGGTTTCTG 660
201 C V Y N G E P W L * 220

661 TAGTAAGTACTAATAGCAAGTAGTTGAATAATAAAAAGATTGTAAGTSCAAAAA 719 ←T7

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FIG. 5

FIG. 5

[illegible]

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Av-HBP

FIG. 6

1	GCGACCGCGCCCAGCCGTACAGAACAAATAGCCTTCGTTGCCAACGTGCAGCGTAGTCGG	60
61	ATGCCTAGTTAAACACCACACACACGTA AAAAGTAGACGAAACTGGCTTCGCTTCCAGCA	120
121	CCAAGCAGGTCATCGTCTGGTCCACTGACGATGAACTCTGCCTTGTGGGTTTTACTAGGA	180
	M N S A L W V L L G	
181	TCATCCTTATGGCTGCATACGGTAGCGTTCATGATTCCCACATGGGCAGATGAAGGCAGG	240
	S S L W L H T V A F M I P T W A D E G R	
241	TTTGGCAAGTACCAGAACGCCTGGAAGGCCCTGAATCAGCGGATTAACACAACACATGTC	300
	F G K Y Q N A W K A L N Q R I <u>N</u> T T H V	
301	CTTGTGAGGTCAACGTATATCGACAATCCATATTTATGGGGCAAGAACTTCTCATGCGTA	360
	L V R S T Y I D N P Y L W G K <u>N</u> F S C V	
361	CGCGCTCGAACTGTCTGAAGTCTTTCCCAGCAGCAAGACTGTGGAAGTGGAGTTTAGTTTC	420
	R A R T V E V F P S S K T V E L E F S F	
421	AGAAACAGGACTGGTATATTGTGCATGAGAAATCAAACGGTTCGAGCTGGAAAGGATTAC	480
	R <u>N</u> R T G I L C M R <u>N</u> Q T V R A G K D Y	
481	TTTTATCATCAGCCTAACGCCTTCGAATTCATGCTGAGAGGTAACAGGTCGTTTTCTAAC	540
	F Y H Q P N A F E F M L R G <u>N</u> R S F S N	
541	GCTGTCATGTTTACCGACGGAATGACATGTAATCTGCTCAGCTTTCCATACCAGCGCAAC	600
	A V M F T D G M T C N L L S F P Y Q R N	
601	AAACCACAATGCGAACTATGGGTGAAGGACACGCGCTCGACAACATTCCCCCTTGTTGC	660
	K P Q C E L W V K D T R V D N I P P C C	
661	TCGTTTCATGTTTCGACTATTTGTGCCCCACAGCCTCGTCCATTCATCATTTACGACAAAGCA	720
	S F M F D Y L C P Q P R P F I I Y D K A	

[illegible]

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721 ATGTGCACGGTGAGGCCACCCCGCTAGAAAGAAAAGGGATGAAAAGGCTACTCGAAGAAG 780
M C T V R P P R *

781 CAACAACCAATCAGTGCCCACAAGAGAACCGTTCCAGTCCTGCGAAAGTTGCGCCTCCCA 840

841 AAACACATACATTTCACTGCAAAGATGACCGATGCAGTCGCAAATTCGTGTCCTAGAACT 900

901 CAAGTGCTGTTTTGGAAACTCGGAAAGGAGACAGTAGAAGCTAACTGCTGTGATACCTAG 960

961 GCCAGGCATTTCCGTCGGGCACTGTTTTTTATGAATAGGGTAGGGTGAAAGTATTTTGGC 1020

1021 TTTGCTGTGGCCCAATAAATAGCGTATATTAGCGGACTAGCATCGAAGTTCAGATGCTA 1080

1081 TAAAGCAGCTAAAACTCACTTCTGCCTGGAACCTCGATAGGTATTGAATAGATCATGCGC 1140

1141 GCACAGAAAAGAAAAGTATCAATCAAAACATAAAAAGCATTCTTCGCATGTGCGCAAAGC 1200

1201 ATTCCCTAAGTCCACGCTAAAAATAGGTGTCATTTTCATATAGCATCGAGTTCTATACGTT 1260

1261 CTTAAGATGCTACCGGTCATTCATTCCTTTCTCGTCTATGCCTCATGGATCTGAACCAAG 1320

1321 TTCTTCTATTGCCTCCTTGTTTTCCGGTAGCTACAGAGTTCAGCAGCACCATTGCTAGTG 1380

1381 CATATTTTATCTTCGTGCTGTGTTTGTCGCAGTATATTTTCTGCCTATTCACGATATTT 1440

1441 GCACAATGTAATAAAACATTTGCCTGCCTAAAAAAAAAAAAAAAAAAAAA 1488

FIG. 6(contd.)

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FIG. 7

lh/Bm-HBP1

1 CTCCAGCTCTGCTTCGACGATGAAGGCTCTCCTGATCGCTGTCGGCTACCTGGCTGCCGT 60
M K A L L I A V G Y L A A V

61 CACAGCGGCACCCCAAGCTTCGCCTTCCTCTCCGAGGAACGAACCACTCAAGAATACTAC 120
T A A P Q A S P S S P R N E P L K N T T

121 GTGGCACAGCAAGGAACTGAAAAATTATCAAGATGCGTGGAAGTCCATCAATCAAAACGT 180
W H S K E L K N Y Q D A W K S I N Q N V

181 CAGCACTACCTACTACTTCCTCAGATCAACCTACAACAACGACAGTGTCTGGGGTAAAAA 240
S T T Y Y F L R S T Y N N D S V W G K N

241 TTTCACCTGTCTTAGCGTCACGGTGACATCGAAACATGAATCAACGTTACCGTCGAATA 300
F T C L S V T V T S K H E S T F T V E Y

301 TAACACCACGTACAAAAATCAGAGCCAACAATGGGTCAGCATGACGGAAAACGTCACGGC 360
N T T Y K N Q S Q Q W V S M T E N V T A

361 CGTGCAGGAGGAGGGCTACGACGTAAAAATATCATTTCAGTGGACAACAGAGAATAACAC 420
V Q E E G Y D V K N I I Q W T T E N N T

421 AAAGTTCAATGATACTGTTGTTTTTACGGACGGCCAGACTTGTGATCTGTTGTACATCCC 480
K F N D T V V F T D G Q T C D L L Y₂ I P

481 GTACAAAGAAAACGGTTACGAGCTGTGGGTGCGTTCCGATTACCTGCAGAACACTCCAAC 540
Y K E N G Y E L W V R S D Y L Q N T P T

541 GTGCTGCCAGTTCATCTTTGACCTCGTCGCATTGGGACGTACCACGTACAATATCTCCAC 600
C C Q F I F D L V A L G R T T Y N I S T

601 TCCTGACTGCGTGACCAAAACCTCTCGTTAGACCGTGAAAGCCGCGGCTTATGCTACTCG 660
P D C V T K T S R *

661 ACTGCTCAGGTTGGAAGAGTAGGGAGCCCCGACGCGCACTACTACTAAAAATGATTCCA 720

721 ATAAGTATTCAAACATTTCAAAAAAAAAAAAAAAAAAAAAA 760

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FIG. 8

lh/Bm-HBP2

1 AGTGACTCCTGCTCTGCTTCGACGATGAAGGCTCTCCTGATCGCTGTCGTCTACCTGACT 60
M K A L L I A V V Y L T

61 GCCGTCACAGCGGCAGACCAAGCTCCGCCTTCTCTACGAGGAATGAACCACTCGAGAAA 120
A V T A A D Q A P P S S T R N E P L E K

121 ACTACCTGGCACAACCAGACACTGGGACGTTATCAAGATGCGTGGAAGTCCATCAATCAA 180
T T W H N Q T L G R Y Q D A W K S I N Q

181 AGCGTCGGCACTACCTACTACTTCCTCAGATCAACCTACAACAACGACAGCGTGTGGGGT 240
S V G T T Y Y F L R S T Y N N D S V W G

241 AAAAATTTACCTGTCTTAGCGTACGGTGACATCGAAATATGAATCAACGTTACCGTC 300
K N F T C L S V T V T S K Y E S T F T V

301 GAATATAACACCACGTACAAAAATCAGAGCCAACAATGGGTCAGCATGTTCGGAACGTC 360
E Y N T T Y K N Q S Q Q W V S M S E N V

361 ACGGCCGTGCAGGAGGGCGGCTACAGTGTTAAAAACATCATTTCAGTGGACAACGGAGAAT 420
T A V Q E G G Y S V K N I I Q W T T E N

421 AACACAAAGTTCAATGATACTGTTGTTTTTACGGACGGCCAGACTTGTGATGTGTTATAC 480
N T K F N D T V V F T D G Q T C D V L Y

481 ATCCCGTACAAAGAAGACGGTTACGAGCTGTGGGTGCGTTCGGAATACCTGCAGAACACT 540
I P Y K E D G Y E L W V R S E Y L Q N T

541 CCAACGTGCTGCCAGTTCATCTTTGACCTCGTCGCATTGGGACGTACCACGTACAATATC 600
P T C C Q F I F D L V A L G R T T Y N I

601 TCCACTCCTAACTGCGTGGCCACCACCGCTGGTTAGACAATGCAAGCCGCGGCTTAATTT 660
S T P N C V A T T A G *

661 ACTCGACCGCTCAGGTTGGAAGTGCCGGGAGCCTCGACGGGCACTACTACTTAAAATGAT 720

721 TTCGAATAAAGTATTCAAGCATTTCTGGAAAAAAAAAAAAAAAAAAAA 765

003160" 95233360

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lh/Bm-HBP-3

1 GATGGCGCTCAGATTGACCTTCTGCTGGCGTGCATCGTCACGGCATGTGGCTGGAGAAC 60
M A L R F A L L A C I V T A C G W R T

61 ACGGATTCAAGAGAAAGGTCCTCCGAGAACACCCCTCTCATGAACACCCACGTTTGGGAAA 120
R I Q E K G P E N N P L M N T Q R L G K

121 AATGCAAGACGCATGGAAGAGTCTGGAAAAGGCAACAATCAGTCGTATGCTTGGTGT 180
M Q D A W K S L E K A T N Q S Y V L V F

181 CCGCTCAAGAAATCACGAACAGAGATATCCTGCGTGTTACGTGAGGCTAGTAATATAAA 240
R S R N H E P E I S C V Y V R A S N I N

241 TAATGACACTAAAACCTGCAACTTATACCAGAACATATTACAATATGACGGCAACGCAAC 300
N D T K T A T Y T R T Y Y N M T A N A T

301 CATGACGGTGAATTATCTGCAAGAGCTCTGAAGCAAGTGGACTATGATCGGAAAAATGT 360
M T V N Y T A R A L K Q V D Y E S E N V

361 CGTACGAGTAAACCTGACAGGTGGGGTCCCCAGCAACGATACAGTTCCTCTTGAAGCTA 420
V R V N L T G G V P S N D T V P L G S Y

421 CGAATACGTCGAGTACGGTAATTACTCTCGAATAGCTCATCGACACCCCTTTTGGATGC 480
E Y V E Y G N Y S C N S S S T P F L D A

481 TGTGCAAAATGGCATCGCAAGGCAATCCAGAGGGCGGATATCGAAGGGCGCACATATCT 540
V Q M A S Q G Q S R G P D I E G R T Y L

FIG. 9

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FIG. 9
(CONTD.)

541 AGACTTCTACGTCGTCATAATCAACCATCGTGCAATGCTCCTGAAGTCCCGCTCCTGGG 600
D F Y V V Y N Q P S C N V L K S P L L G

601 AGGTGCTGTGACTTTTGGGTGACAGATCCGAGTTGCAAAAAGCACTAAATAAGACATC 660
G A C D F W V T E S E L Q K A L N K T S

661 AGAGAGAAAAAACAAGCTAGAAAGCGAGAGCAAGAAAGCTGGAGGAGATTCCGATGA 720
E K K K T K L E A R A R K A G G D S D D

721 CCAGGGACCTGAACCTGAGGTGCTTCAAAAAATCTGCCCCCTCCTGCCGCGCAGCGTT 780
Q G P E L E V V F K N L P P P C R A A F

781 CATAACTTCCTGGGGCTATCCAACCTTTTCTTATGTACAACAAGACCATCTGTAAATCGAAC 840

I T S C G Y P T F L M Y N K T I C N R T

841 GGATTCTGCTGCGGTGTGAACGTCCTCCCTGCGAGCAAGTAGAACGTCCTGTAAGACAGCAG 900
D S A A V *

901 GAAGATAGTTGACTGTTTGTGGCGGAATGTGACTACTAGTCTGAATCATTTAAAAAGAT 960

961 TCNGCTGACGGGTGTGGCGGGAACCTTTTAAATGAAATTTGGTCATCTACTTGTGAAAGAC 1020

1021 AAAAATAAAACAATATGTTACTCCTC 1046

Ih/Bm-HBP4

FIG. 10

1	GGAAACCAGGATGGCGCTCAGATTTGCACTTCTGCTGGCGTGCATCGTCACGGCATGTGG M A L R F A L L L A C I V T A C G	60
61	CTGGAGAACACGGATTCAAGAGAAAGGTCCCGAGAACAACCCTCTCATGAACACCCAACG W R T R I Q E K G P E N N P L M N T Q R	120
121	TTTGGGAAAAATGCAAGACGCATGGAAGAGTCTGGAAAAGGCAGCAAATCAGACGTATGT L G K M Q D A W K S L E K A A <u>N</u> Q T Y V	180
181	CTTGGTGTTCCGCTCAAGAAATCACGAACCAGATATATCCTGCGTCTACGTGAGAGCTAG L V F R S R N H E P D I S C V Y V R A S	240
241	TAATTTAGATAATGCAACTAAAACTGCAGATTATACCAGAACATATTACAATATGACGGC N L D <u>N</u> A T K T A D Y T R T Y Y <u>N</u> M T A	300
301	AAAACAAAACGTGTCGGTAAATTATACTGCAAGAGCTCTGAAGCAAGTGGACTATGAGTC K Q <u>N</u> V S V <u>N</u> Y T A R A L K Q V D Y E S	360
361	GGAAAATGTCGTACGAGTAAACCTGACAGGTGGGGTCCCCAGTAACGATACAGTTCCTCC E N V V R V <u>N</u> L T G G V P S <u>N</u> D T V P P	420
421	TGGAAGCTTCGAATACGTGAGTACGGTAATTACTCCTGCAATAGCTCATCGACACCCTT G S F E Y V E Y G <u>N</u> Y S C <u>N</u> S S S T P F	480
481	TTTGGATGCTGTGCAAATGGCATCGCAAGGGCAATCCTGGGGGCCGGATGTGCAAGGGCG L D A V Q M A S Q G Q S W G P D V E G R	540

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541 CACATATCTAGATTTCTACGTCGTCTACAATCAACCGTCGTGCAATGTCCTGAAGTCCCC 600
T Y L D F Y V V Y N Q P S C N V L K S P

601 GCTCCTGGGAGGTGCTTGTGACTTCTGGGTGCCACAATCAGAGTTGGACAAGGTACTAA 660
L L G G A C D F W V P Q S E L D K V L N

661 CAAAAAAGGAGATAAGAAAAAGCCAGCTAAGTCAAGCAGTCAAAATGGAGACGAAGGTT 720
K K G D K K K P A K S S S Q N G D E G S

721 TGATGCCGAGCAACCTGAACTGGAGGCCATCTTTAAACATCTACCCCCTCCCTGCCGCG 780
D A E Q P E L E A I F K H L P P P C R A

781 AGCGTTCATAACTTCCTGCGGCTATCCAAATTTTCTCATGTACAACAAGACGATCTGTAA 840
A F I T S C G Y P N F L M Y N K T I C N

841 TGCAGCGGGTCATGCTGCGAACTGAACGTCCCTCTGCGAACGAGTAGAGCGTGCGTAAAA 900
A A G H A A N *

901 CAACTGGTCTGAATCTTTTAAGAAATTTCGGCAAAGTGCGGGTGGCGCGAACTTTTATCAA 960

961 ACTGGTCATACATGTGAAAGAAAAAAATAAACAAAATGTGCATAAAAAAAAAAAAAAAA 1020

1021 AAAAA 1025

FIG. 10(contd.)

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00CT60" 96255560

541 AAATATGATGAAATGCCCGGATGCCGAAATTTTTCGACAATTTTATTGGTGCT 600
K Y D E M P R D G R N Y L F D N F I G A

601 TACTTGGACTTCTACGTGGTGTTCAGCCAGCCGACATGCAACGTTCTCAGAGTCCGAGAA 660
Y L D F Y V V F S Q P T C N V L R V R E

661 GGATGTGACTTCTGGCTAAGGAAACTGAGTTGCCAAGCCTACTGAAAGCAGAGAAAT 720
G C D F W L R K T E L P S L L K A A E N

721 GATGACAACGATAACCGAATCGTGAAGAAGTATTTGGAAAGAAATAATAATACT 780
D D N D N T E S L K N Y W E R R I N N T

781 AAAACAAGATTTTCGACATAATACTAAGAAATGTAAGATGTACGTACAACGTTATTCAATT 840
K T R F R H N T K K C K M Y V Q R Y S I

841 GAGAAGGCTGAAGATGTCTTTAAAAACACTGCTTTTAAACACCTCCCTCCGACTGCCGC 900
E K A E D V F K N T A F K H L P S D C R

901 TTTGCCCTTCCTGGCCGCTTGTTGGAATCCAGCATTCACAATATACGACCCAGAAACATGT 960
F A F L A A C G N P A F T I Y D P E T C

961 AATAGCTCCCTGCCAGCTAATATGGCAGAAAGTTAAATGAGCTATTTTCATCTTCGTCG 1020
N S S L P A N M A E S *

1021 ACCGTATGCCCTGGTATGCAAGAAGGTGAGGTGGACAGGATACTTCCGAATTATTTTTC 1080

1081 AGTCTGCCCTTGACGCACGAAATAACAAAATATCTGTTGAAGCCNCAACNNNNNNNAANA 1140

1141 ANAAAAAAAAAAAAA 1156

FIG. 11
(CONTD.)

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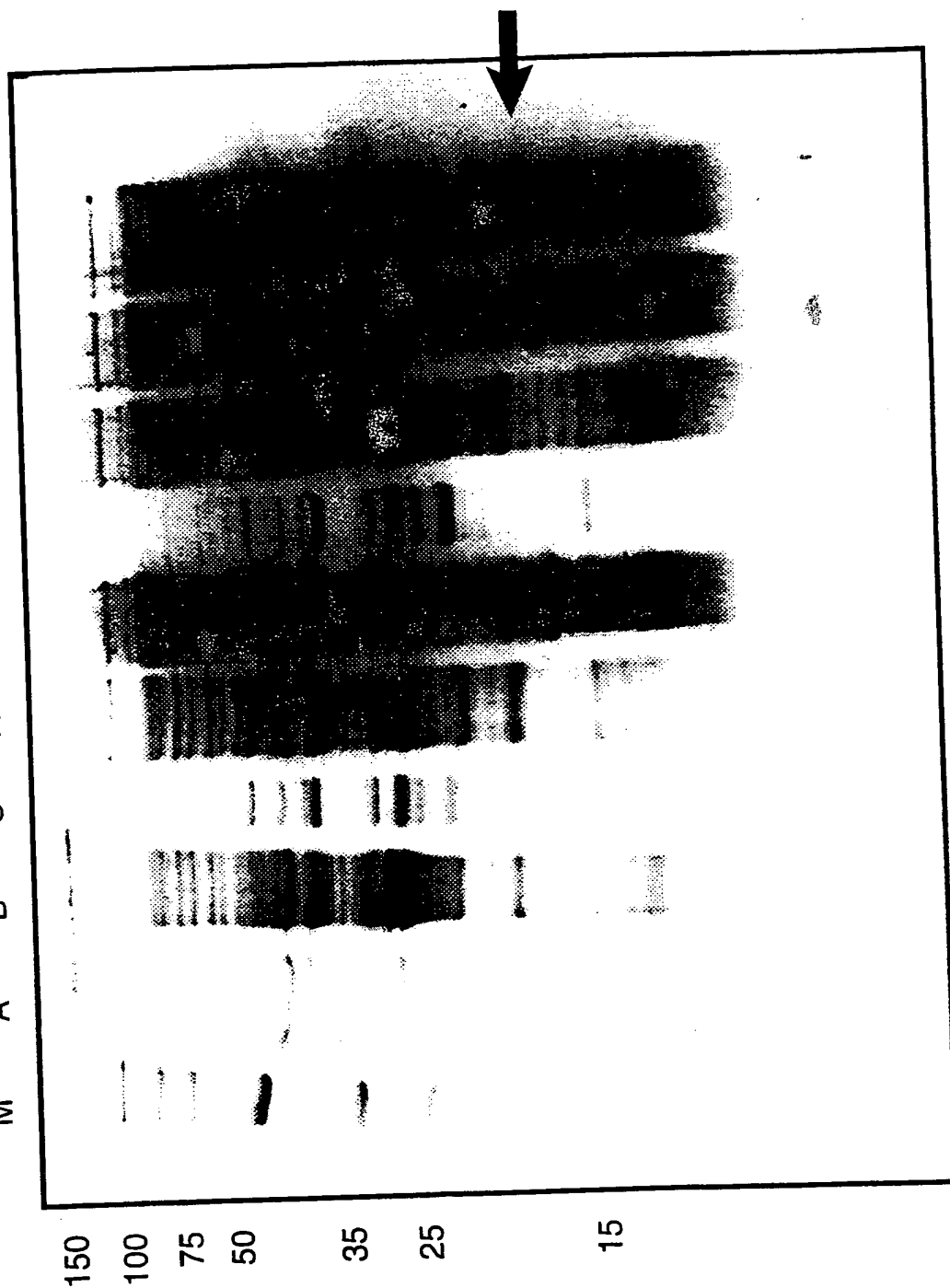
TIME COURSE
OF EXPRESSION
(HOUR)

POST-IPTG
INDUCTION

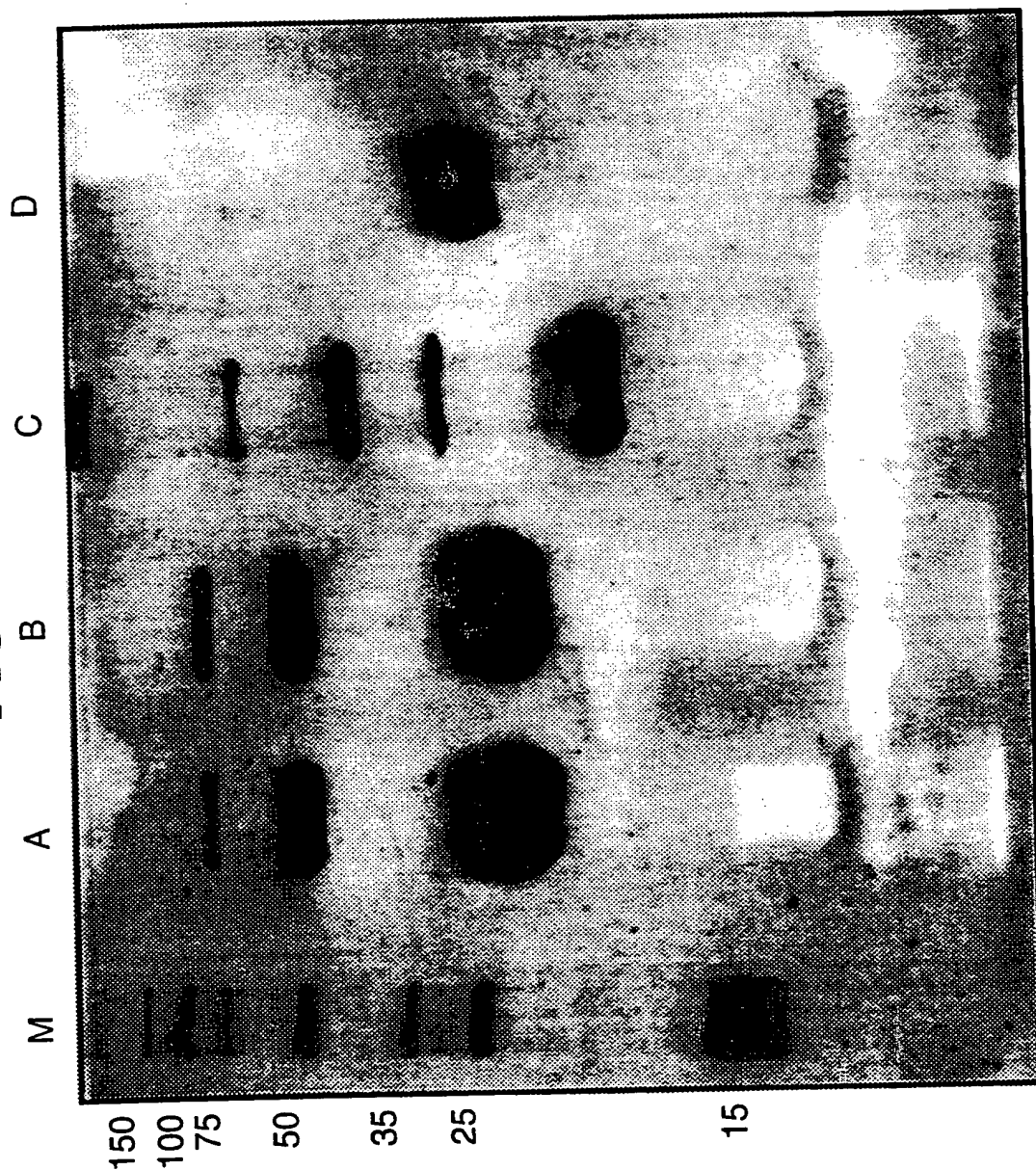
PRE-IPTG
INDUCTION

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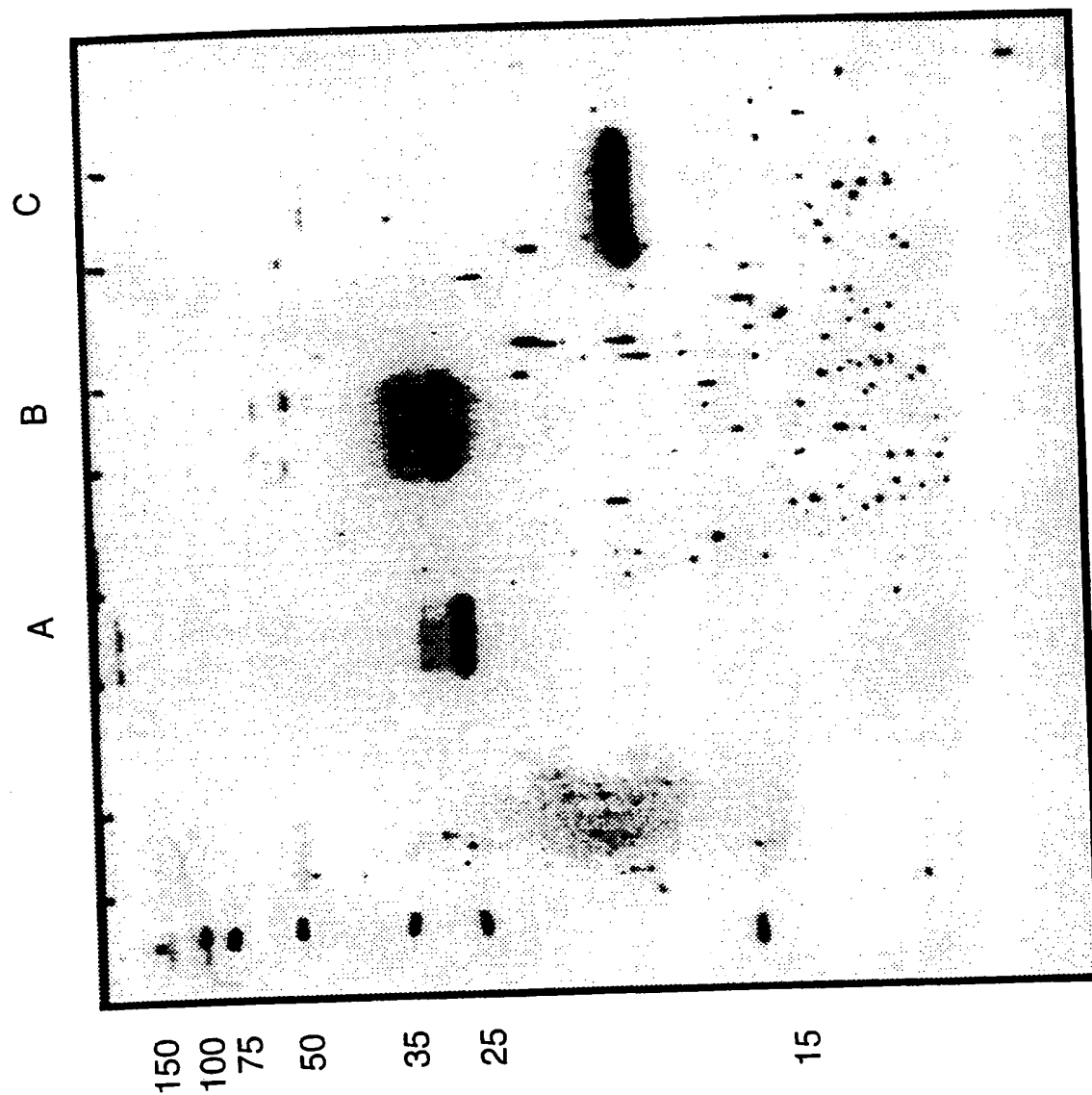
FIG. 12



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FIG. 13

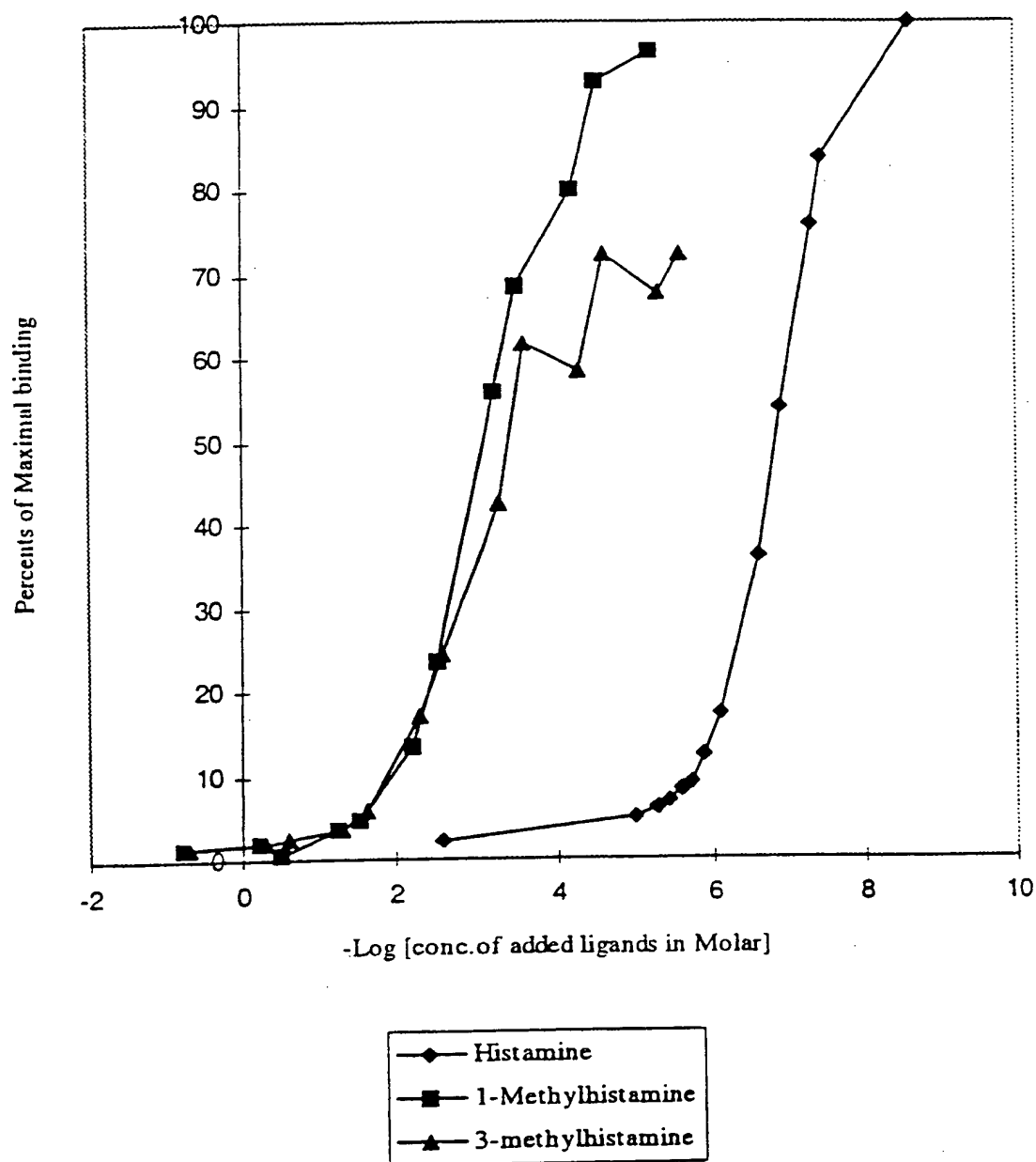
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FIG. 15

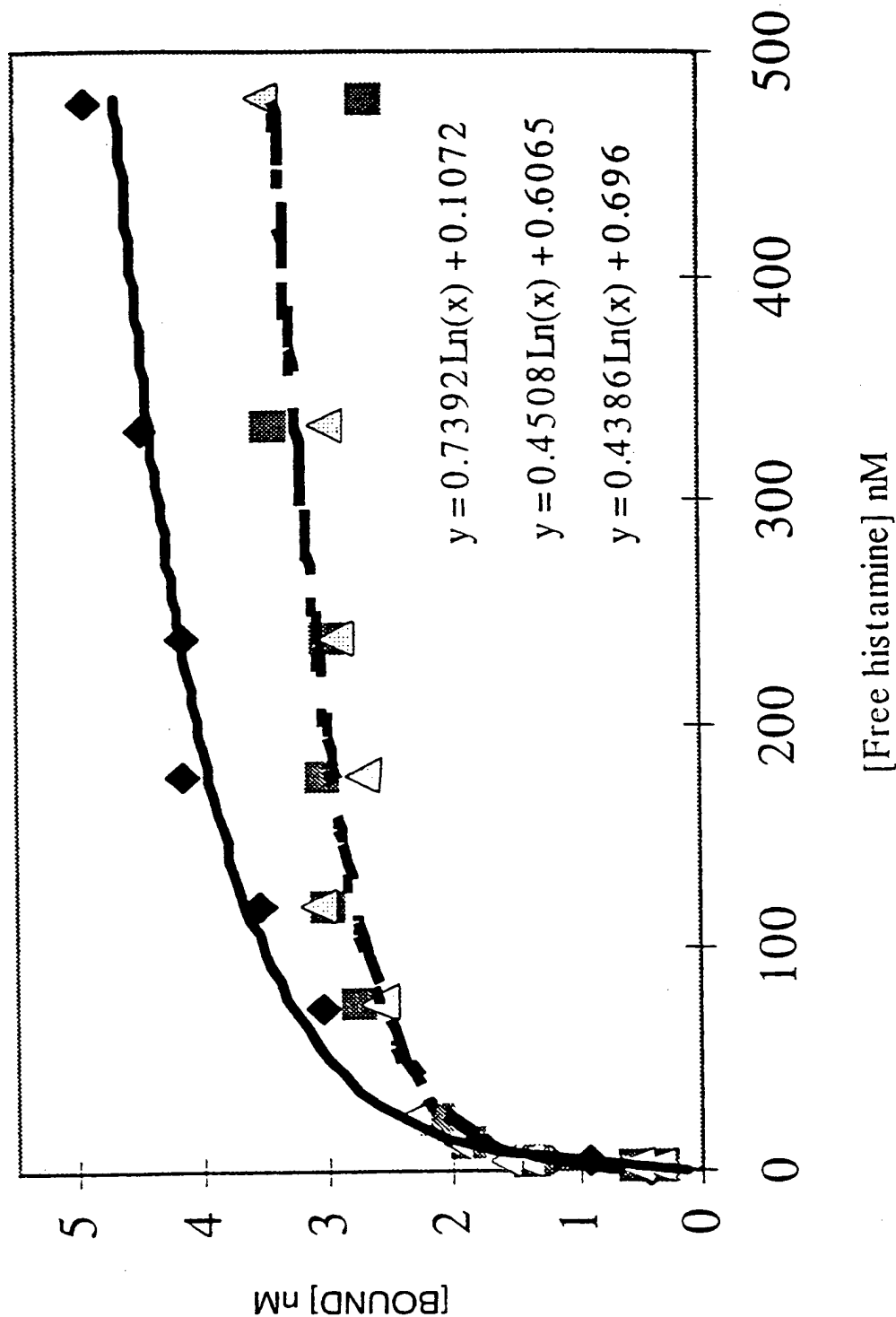
Binding Activity of derretine to histamine and its methylsubstitutions



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Histamine-binding saturation curve

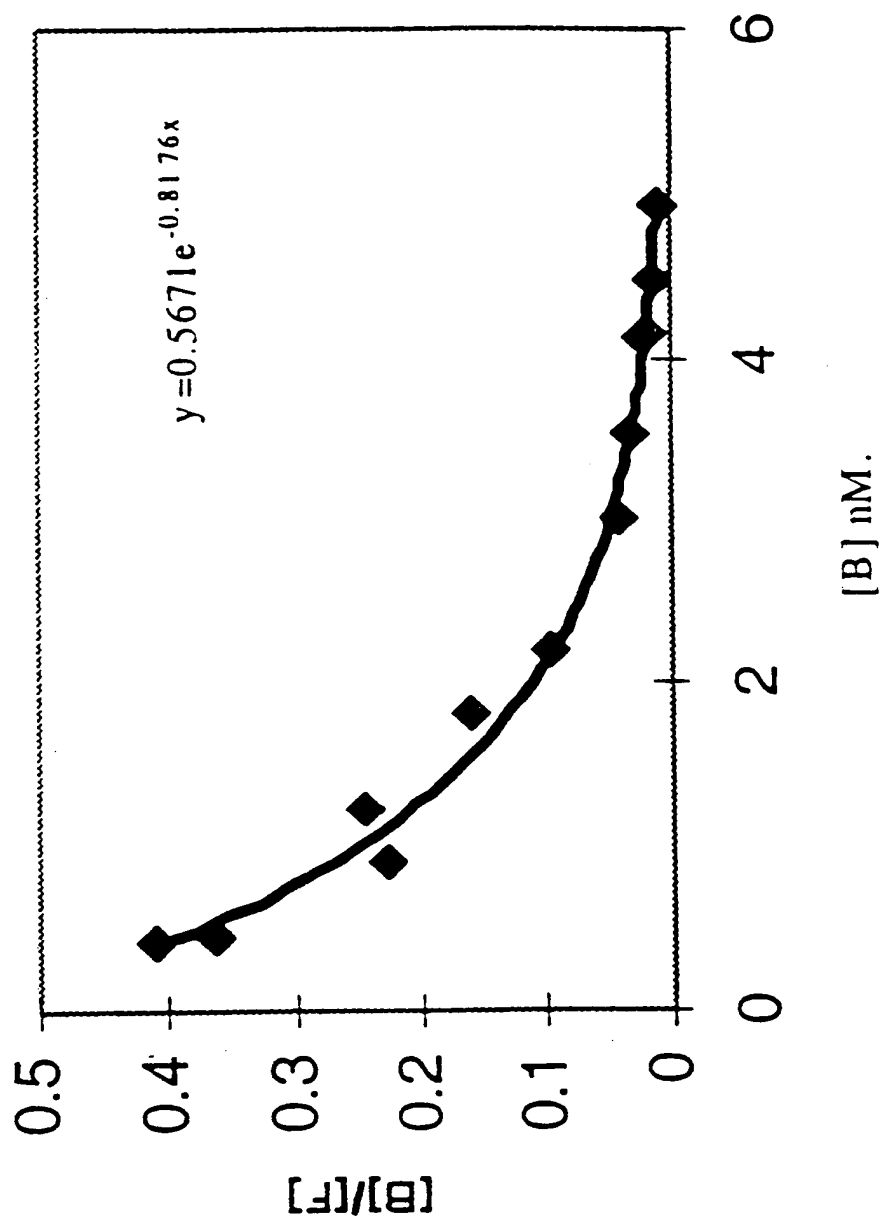
FIG. 16



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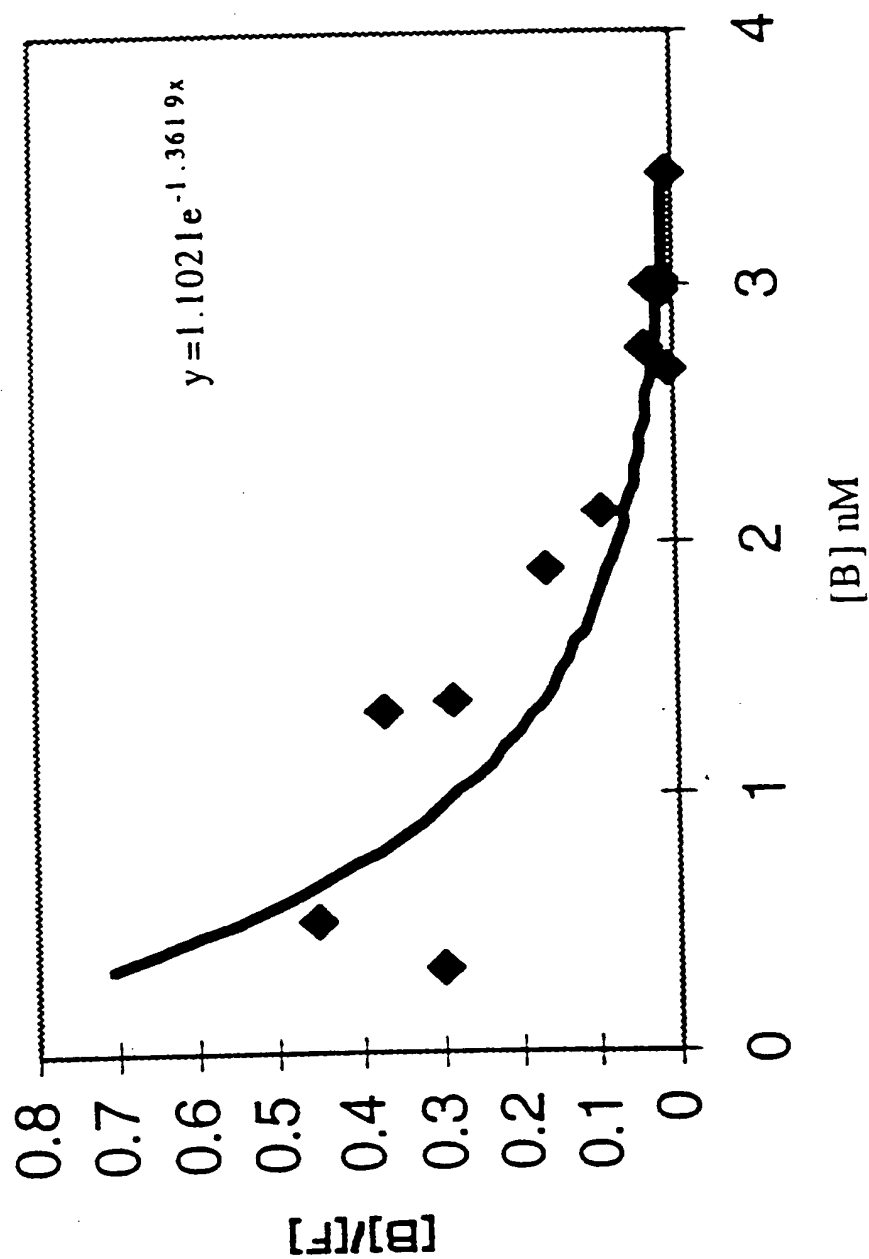
Scatchard (without 5-HT)

FIG. 17



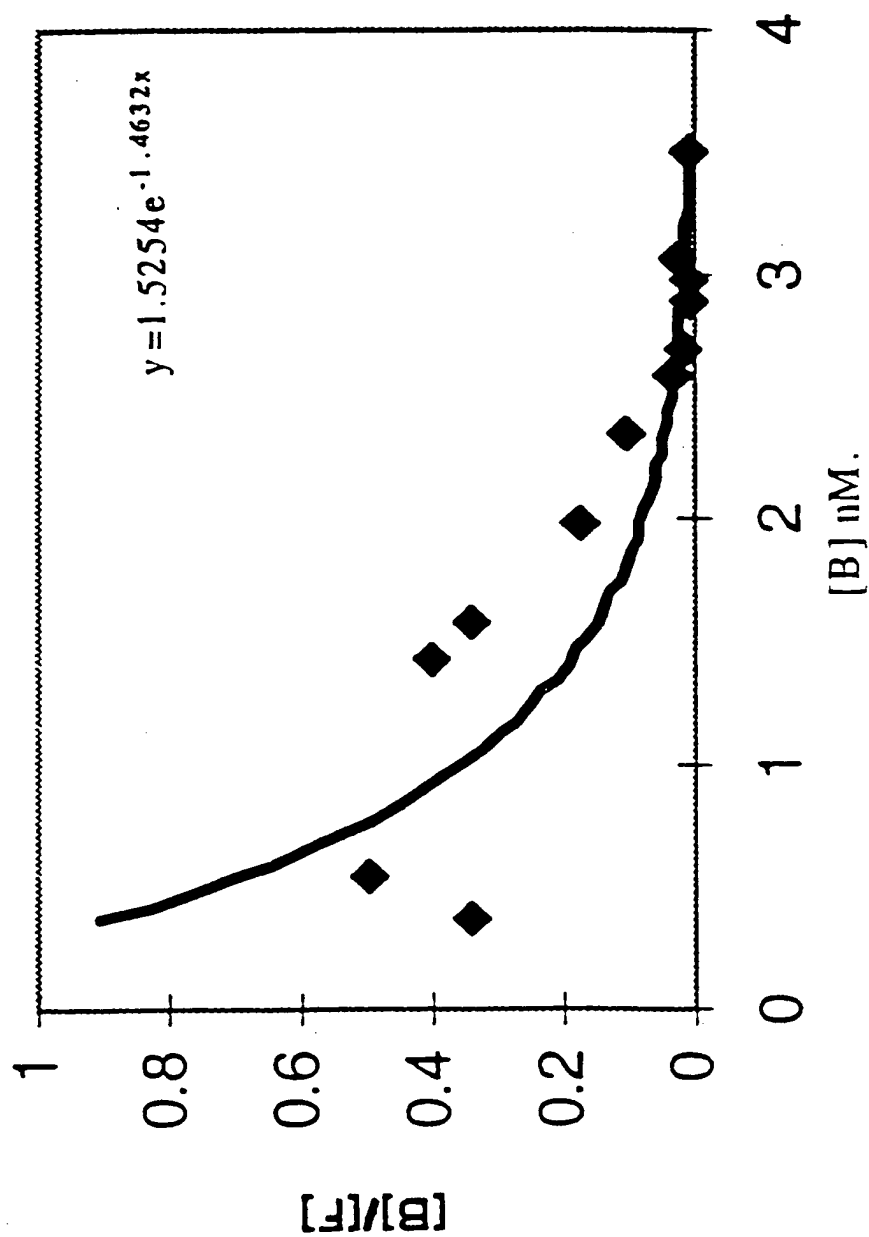
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FIG. 17(contd.)
Scatchard (+2.38 mM 5-HT)



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FIG. 17(contd.) Scatchard (+23.8 nM 5-HT)



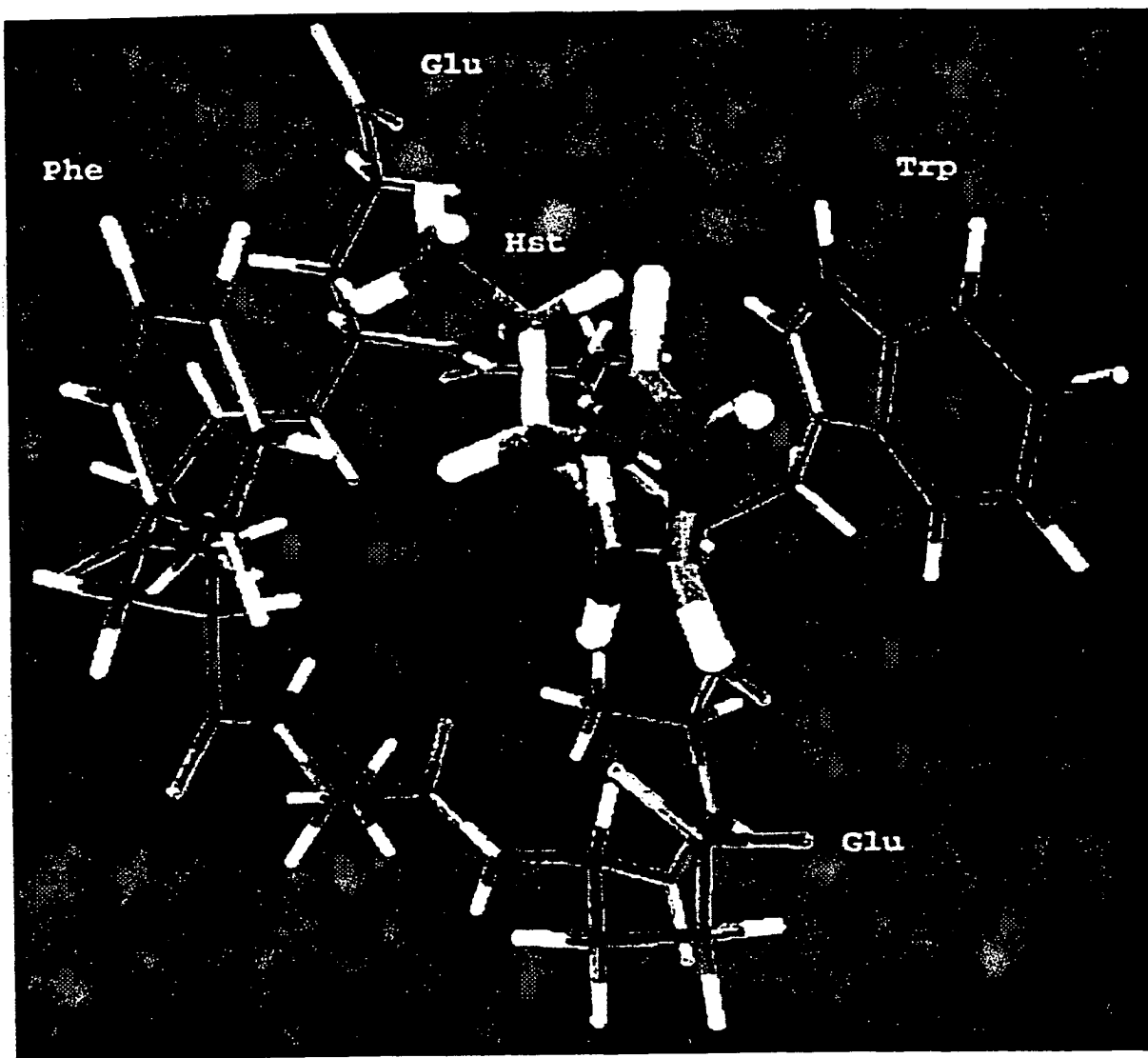
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FIG. 18

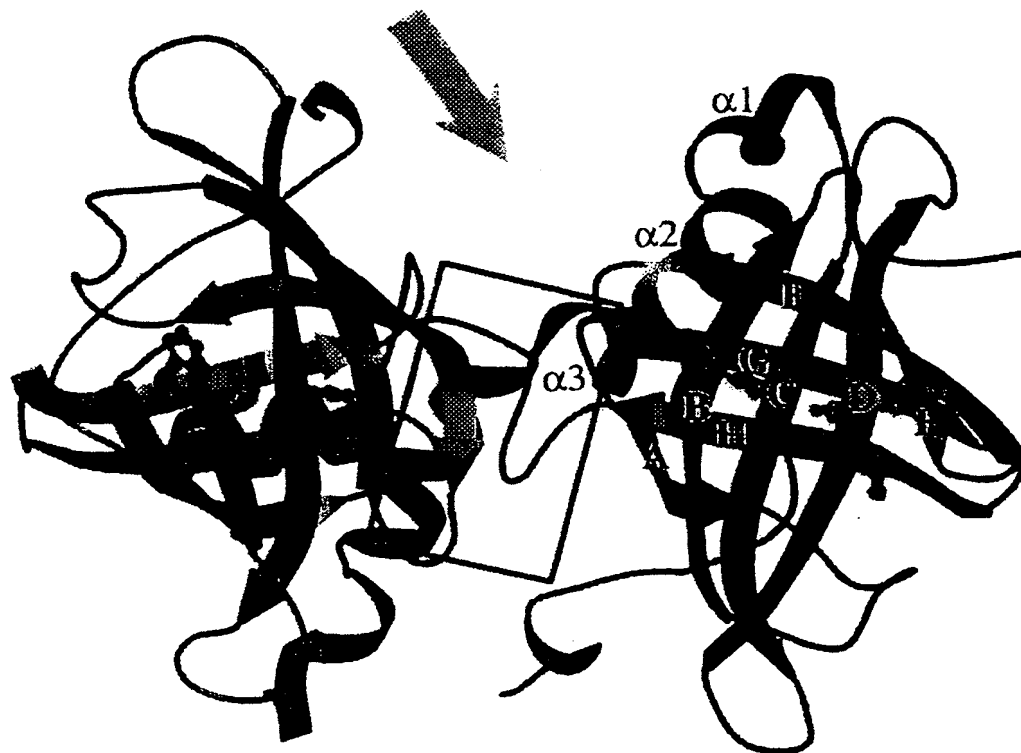
005160" 00225550

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FIG. 19

09555296.091300

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FIG. 20(a)**FIG. 20(b)**

PCT 60 " 3624560

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FIG. 20(c)

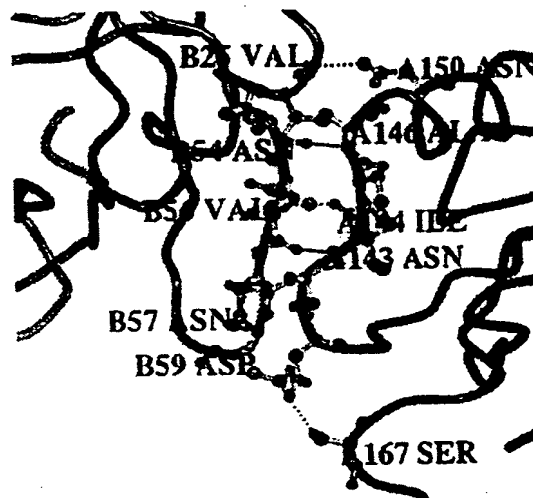
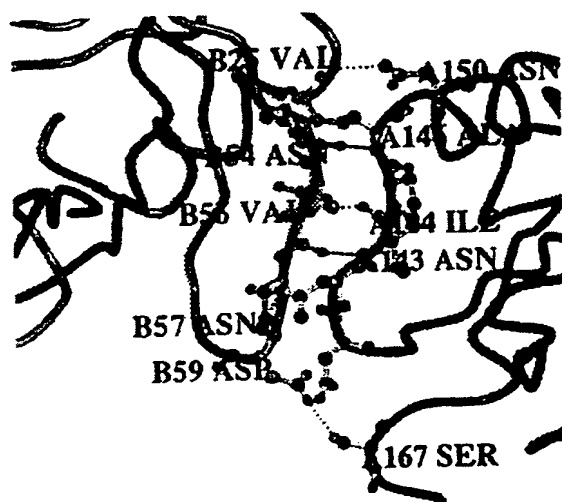
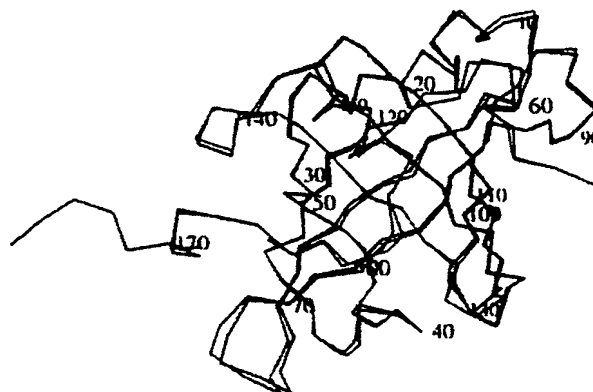
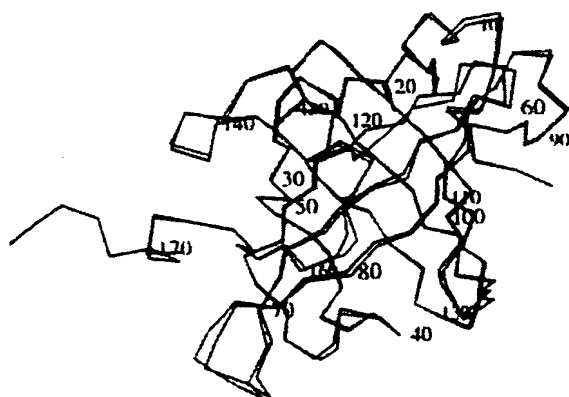


FIG. 20(d)



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FIG. 21(a)

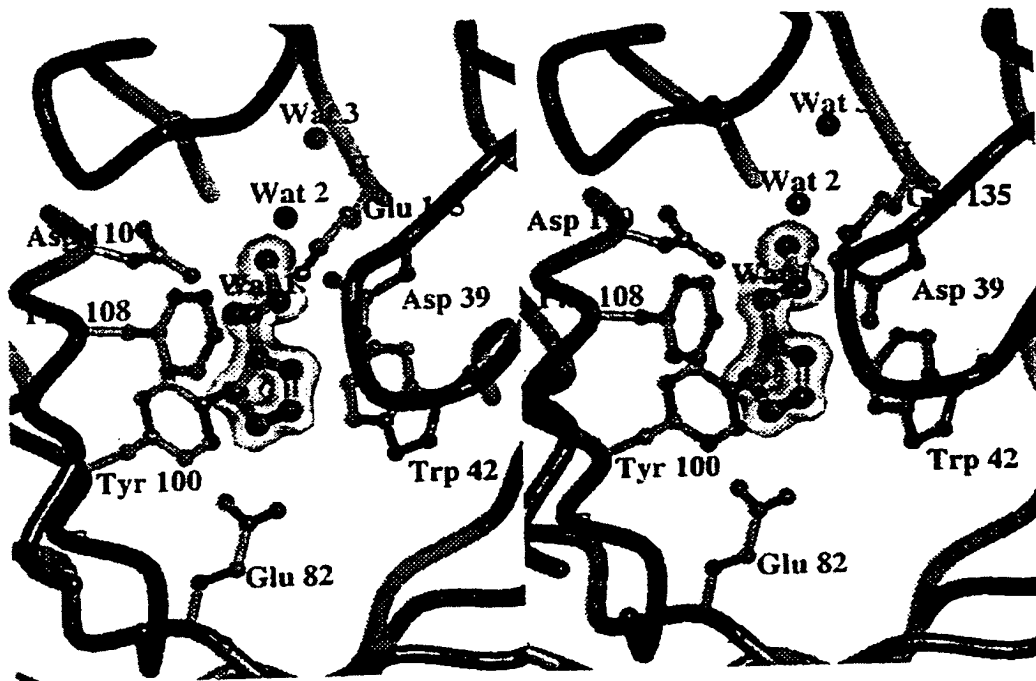


FIG. 21(b)



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FIG. 21(c)

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[illegible][illegible]

FIG. 22

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ihhbp3	LDAV	-	-	-	Q	M	A	S	Q	Q	Q	S	R	G	P	D	I	E	G	R	T	Y	L	D	F	F	Y	V	V	Y	N	Q	P	S	C	N	V	L	-	-	-	-	K	S	P	L	L	G	G	A	C	203		
ihhbp4	LDAV	-	-	-	-	Q	M	A	S	Q	Q	Q	S	R	G	P	D	V	E	G	R	T	Y	L	D	F	F	Y	V	V	Y	N	Q	P	S	C	N	V	L	-	-	-	-	K	S	P	L	L	G	G	A	C	203	
ihhbp5	SNGI	S	A	K	Y	D	E	M	P	R	D	G	R	N	Y	L	F	D	N	F	I	G	A	Y	L	D	F	F	Y	V	V	F	S	Q	P	T	C	N	V	L	-	-	-	-	R	-	-	-	V	R	E	G	C	212
FS-HBP1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	G	Q	V	L	T	D	V	L	A	F	S	D	-	D	N	C	Y	V	I	I	A	L	G	P	D	G	S	G	A	-	Y	152		
FS-HBP2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	G	Q	V	F	T	D	V	I	A	F	S	D	-	D	N	C	D	V	I	I	V	P	P	T	D	G	N	E	E	G	-	Y	153	
MS-HBP1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	R	Q	T	F	E	N	D	V	F	F	S	D	-	D	N	C	D	V	I	I	F	V	P	K	E	R	G	S	D	E	G	Y	153	
ihhbp1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	N	T	K	F	E	N	D	T	V	V	F	T	D	G	Q	T	C	D	L	L	Y	I	P	Y	K	E	N	-	-	G	-	-	Y	160
ihhbp2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	N	T	K	F	E	N	D	T	V	V	F	T	D	G	Q	T	C	D	V	L	Y	I	P	Y	K	E	N	-	-	G	-	-	Y	160
D.RET6	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	G	L	N	I	T	D	T	L	I	F	T	D	G	E	L	C	D	V	F	Y	V	P	N	A	D	Q	-	-	G	-	-	C	163	
avhbp	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	N	R	S	F	E	N	A	V	M	F	T	D	G	M	T	C	N	L	L	S	F	P	Y	Q	R	N	K	P	Q	-	-	C	154	
ra-res	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	V	N	S	I	G	P	V	R	S	N	S	E	N	P	P	E	R	L	T	A	S	Q	E	S	A	Q	R	D	C	164				

ihhbp3	D F W V	T E S E L Q K A L	- - - - -	- - - - -	N K T S E K K K T K L E A R A R K A G	- - - - -	235
ihhbp4	D F W V	P Q S E L D K V L	- - - - -	- - - - -	N K K G D K K K P A - K S S S Q N G D	- - - - -	234
ihhbp5	D F W L	R K T E L P S L L K A A E N D D N D N T E S L K N Y W E R R I N N T K T R F R H N T K K C K M Y V Q R Y	- - - - -	- - - - -	- - - - -	- - - - -	268
FS-HBP1	E L W A T D	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	158
FS-HBP2	E L W T T D	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	159
MS-HBP1	E L W V S E D K	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	161
ihhbp1'	E L W V R S D Y	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	168
ihhbp2	E L W V R S E Y	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	168
D.RET6	E L W V K K S H	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	171
avhbp	E L W V K D T R	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	162
ra-res	V L W V D H D E K A T O	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	176

ihhbp3	G	D	S	D	D	Q	G	P	E	L	E	V	V	F	K	N	L	P	P	P	P	P	C	R	A	A	F	I	T	S	C	G	Y	P	T	F	L	M	Y	N	K	T	I	C	N	-	-	R	T	D	S	A	A	V	285		
ihhbp4	E	G	S	D	A	E	Q	P	E	L	E	A	I	F	K	H	L	P	P	P	P	P	C	R	A	A	F	I	T	S	C	G	Y	P	T	F	L	M	Y	N	K	T	I	C	N	-	-	A	A	G	H	A	A	N	284		
ihhbp5	S	I	E	K	A	E	D	V	F	K	N	T	A	F	K	H	L	P	P	P	P	P	C	R	E	F	A	F	L	A	A	C	G	N	P	A	F	T	I	Y	D	P	E	T	C	N	S	S	L	P	A	N	M	A	E	S	321
FS-HBP1	-	-	-	-	-	-	-	-	-	Y	T	D	V	P	A	S	C	L	E	K	F	N	E	Y	A	A	G	L	P	-	-	V	R	D	-	-	V	Y	T	-	-	-	-	S	D	C	L	P	E	190							
FS-HBP2	-	-	-	-	-	-	-	-	-	Y	D	N	I	P	A	N	C	L	N	K	F	N	E	Y	A	A	G	R	E	-	-	T	R	D	-	-	T	R	D	-	-	V	F	T	-	-	S	A	C	L	-	E	190				
MS-HBP1	-	-	-	-	-	-	-	-	-	I	D	K	I	P	P	D	C	C	K	F	T	M	A	Y	F	A	Q	Q	E	K	T	V	R	N	-	-	V	Y	T	D	S	S	C	K	P	A	P	A	Q	N	200						
ihhbp1	-	-	-	-	-	-	-	-	-	L	Q	N	T	P	T	C	C	Q	F	I	F	D	-	L	V	A	-	L	G	R	T	T	Y	N	-	-	I	S	T	P	D	C	V	T	K	T	S	R	-	-	203						
ihhbp2	-	-	-	-	-	-	-	-	-	L	Q	N	T	P	T	C	C	Q	F	I	F	D	-	L	V	A	-	L	G	R	T	T	Y	N	-	-	I	S	T	P	D	C	V	A	T	T	A	G	-	-	203						
D.RET6	-	-	-	-	-	-	-	-	-	Y	K	H	V	P	P	D	Y	C	F	F	V	F	N	V	F	C	A	-	K	D	R	K	T	Y	D	-	-	I	F	N	E	E	C	V	Y	N	G	E	P	W	L	209					
avhbp	-	-	-	-	-	-	-	-	-	V	D	N	I	P	P	C	C	S	F	F	D	Y	L	C	P	-	Q	P	R	P	F	-	-	I	Y	D	K	A	M	C	T	V	R	P	P	R	198										
ra-res	-	-	-	-	-	-	-	-	-	-	-	-	-	E	O	C	C	E	D	F	F	K	T	H	C	K	E	T	V	H	V	I	Y	D	V	N	R	C	-	-	-	-	-	K	E	N	G	S	E	207							

FIG. 22(Contd.)